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RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/09/994,185

TIME: 11:40:03

Input Set : N:\Crf3\RULE60\09994185.raw

Output Set: N:\CRF3\01282002\I994185.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: White, Mark Leslie

3 Carroll, Stephen Fitzhugh

4 Ma, Jeremy Kam-kuen

5 (ii) TITLE OF INVENTION: METHOD FOR QUANTIFYING LBP IN BODY FLUIDS

6 (iii) NUMBER OF SEQUENCES: 4

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

9 (B) STREET: 6300 Sears Tower, 233 South Wacker Drive

10 (C) CITY: Chicago

11 (D) STATE: Illinois

12 (E) COUNTRY: United States of America

13 (F) ZIP: 60606-6402

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk

16 (B) COMPUTER: IBM PC compatible

17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

18 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/09/994,185

C--> 21 (B) FILING DATE: 26-Nov-2001

22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:

24 (A) APPLICATION NUMBER: 09/286,153

25 (B) FILING DATE:

26 (viii) ATTORNEY/AGENT INFORMATION:

27 (A) NAME: Lin-Laures, Li-Hsien

28 (B) REGISTRATION NUMBER: 33,547

29 (C) REFERENCE/DOCKET NUMBER: 27129/33783

30 (ix) TELECOMMUNICATION INFORMATION:

31 (A) TELEPHONE: 312/474-6300

32 (B) TELEFAX: 312/474-0448

33 (C) TELEX: 25-3856

34 (2) INFORMATION FOR SEQ ID NO: 1:

35 (i) SEQUENCE CHARACTERISTICS:

36 (A) LENGTH: 1443 base pairs

37 (B) TYPE: nucleic acid

38 (C) STRANDEDNESS: single

39 (D) TOPOLOGY: linear

W--> 40 (ii) MOLECULE TYPE: DNA

41 (ix) FEATURE:

42 (A) NAME/KEY: CDS

ENTERED

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43      (B) LOCATION: 1..1443
44  (ix) FEATURE:
45      (A) NAME/KEY: mat_peptide
46      (B) LOCATION: 76..1443
47  (ix) FEATURE:
48      (A) NAME/KEY: misc_feature
49      (D) OTHER INFORMATION: "rLBP"
50  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51  ATG GGG GCC TTG GCC AGA GCC CTG CCG TCC ATA CTG CTG GCA TTG CTG      48
52  Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
53  -25                      -20                      -15                      -10
54  CTT ACG TCC ACC CCA GAG GCT CTG GGT GCC AAC CCC GGC TTG GTC GCC      96
55  Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
56                      -5                      1                      5
57  AGG ATC ACC GAC AAG GGA CTG CAG TAT GCG GCC CAG GAG GGG CTA TTG      144
58  Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
59                      10                      15                      20
60  GCT CTG CAG AGT GAG CTG CTC AGG ATC ACG CTG CCT GAC TTC ACC GGG      192
61  Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
62  25                      30                      35
63  GAC TTG AGG ATC CCC CAC GTC GGC CGT GGG CGC TAT GAG TTC CAC AGC      240
64  Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
65  40                      45                      50                      55
66  CTG AAC ATC CAC AGC TGT GAG CTG CTT CAC TCT GCG CTG AGG CCT GTC      288
67  Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
68                      60                      65                      70
69  CCT GGC CAG GGC CTG AGT CTC AGC ATC TCC GAC TCC TCC ATC CGG GTC      336
70  Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
71                      75                      80                      85
72  CAG GGC AGG TGG AAG GTG CGC AAG TCA TTC TTC AAA CTA CAG GGC TCC      384
73  Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser
74  90                      95                      100
75  TTT GAT GTC AGT GTC AAG GGC ATC AGC ATT TCG GTC AAC CTC CTG TTG      432
76  Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu
77  105                      110                      115
78  GGC AGC GAG TCC TCC GGG AGG CCC ACA GTT ACT GCC TCC AGC TGC AGC      480
79  Gly Ser Glu Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser
80  120                      125                      130                      135
81  AGT GAC ATC GCT GAC GTG GAG GTG GAC ATG TCG GGA GAC TTG GGG TGG      528
82  Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp
83  140                      145                      150
84  CTG TTG AAC CTC TTC CAC AAC CAG ATT GAG TCC AAG TTC CAG AAA GTA      576
85  Leu Leu-Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val
86  155                      160                      165
87  CTG GAG AGC AGG ATT TGC GAA ATG ATC CAG AAA TCG GTG TCC TCC GAT      624
88  Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp
89  170                      175                      180
90  CTA CAG CCT TAT CTC CAA ACT CTG CCA GTT ACA ACA GAG ATT GAC AGT      672
91  Leu Gln Pro Tyr Leu Gln Thr Leu Pro Val Thr Thr Glu Ile Asp Ser

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92	185	190	195	
93	TTC GCC GAC ATT GAT TAT AGC TTA GTG GAA GCC CCT CGG GCA ACA GCC			720
94	Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala			
95	200	205	210	215
96	CAG ATG CTG GAG GTG ATG TTT AAG GGT GAA ATC TTT CAT CGT AAC CAC			768
97	Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His			
98		220	225	230
99	CGT TCT CCA GTT ACC CTC CTT GCT GCA GTC ATG AGC CTT CCT GAG GAA			816
100	Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu			
101		235	240	245
102	CAC AAC AAA ATG GTC TAC TTT GCC ATC TCG GAT TAT GTC TTC AAC ACG			864
103	His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr			
104		250	255	260
105	GCC AGC CTG GTT TAT CAT GAG GAA GGA TAT CTG AAC TTC TCC ATC ACA			912
106	Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe Ser Ile Thr			
107		265	270	275
108	GAT GAG ATG ATA CCG CCT GAC TCT AAT ATC CGA CTG ACC ACC AAG TCC			960
109	Asp Glu Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser			
110		280	285	290
111	TTC CGA CCC TTC GTC CCA CGG TTA GCC AGG CTC TAC CCC AAC ATG AAC			1008
112	Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn			
113		300	305	310
114	CTG GAA CTC CAG GGA TCA GTG CCC TCT GCT CCG CTC CTG AAC TTC AGC			1056
115	Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser			
116		315	320	325
117	CCT GGG AAT CTG TCT GTG GAC CCC TAT ATG GAG ATA GAT GCC TTT GTG			1104
118	Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val			
119		330	335	340
120	CTC CTG CCC AGC TCC AGC AAG GAG CCT GTC TTC CGG CTC AGT GTG GCC			1152
121	Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala			
122		345	350	355
123	ACT AAT GTG TCC GCC ACC TTG ACC TTC AAT ACC AGC AAG ATC ACT GGG			1200
124	Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly			
125		360	365	370
126	TTC CTG AAG CCA GGA AAG GTA AAA GTG GAA CTG AAA GAA TCC AAA GTT			1248
127	Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val			
128		380	385	390
129	GGA CTA TTC AAT GCA GAG CTG TTG GAA GCG CTC CTC AAC TAT TAC ATC			1296
130	Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile			
131		395	400	405
132	CTT AAC ACC TTC TAC CCC AAG TTC AAT GAT AAG TTG GCC GAA GGC TTC			1344
133	Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe			
134		410	415	420
135	CCC CTT CCT CTG CTG AAG CGT GTT CAG CTC TAC GAC CTT GGG CTG CAG			1392
136	Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln			
137		425	430	435
138	ATC CAT AAG GAC TTC CTG TTC TTG GGT GCC AAT GTC CAA TAC ATG AGA			1440
139	Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg			
140	440	445	450	455

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Input Set : N:\Crif3\RULE60\09994185.raw

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141 GTT
 142 Val 1443
 144 (2) INFORMATION FOR SEQ ID NO: 2:
 145 (i) SEQUENCE CHARACTERISTICS:
 146 (A) LENGTH: 481 amino acids
 147 (B) TYPE: amino acid
 148 (D) TOPOLOGY: linear
 149 (ii) MOLECULE TYPE: protein
 150 (ix) FEATURE:
 151 (A) NAME/KEY: misc_feature
 152 (D) OTHER INFORMATION: "rLBP"
 153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 154 Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
 155 -25 -20 -15 -10
 156 Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
 157 -5 1 5
 158 Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
 159 10 15 20
 160 Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
 161 25 30 35
 162 Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
 163 40 45 50 55
 164 Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
 165 60 65 70
 166 Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
 167 75 80 85
 168 Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser
 169 90 95 100
 170 Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu
 171 105 110 115
 172 Gly Ser Glu Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser
 173 120 125 130 135
 174 Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp
 175 140 145 150
 176 Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val
 177 155 160 165
 178 Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp
 179 170 175 180
 180 Leu Gln Pro Tyr Leu Gln Thr Leu Pro Val Thr Thr Glu Ile Asp Ser
 181 185 190 195
 182 Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala
 183 200 205 210 215
 184 Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His
 185 220 225 230
 186 Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu
 187 235 240 245
 188 His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr
 189 250 255 260
 190 Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe Ser Ile Thr

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191      265      270      275
192  Asp Glu Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser
193      280      285      290      295
194  Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn
195      300      305      310
196  Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser
197      315      320      325
198  Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val
199      330      335      340
200  Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala
201      345      350      355
202  Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly
203      360      365      370      375
204  Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val
205      380      385      390
206  Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile
207      395      400      405
208  Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe
209      410      415      420
210  Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln
211      425      430      435
212  Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg
213      440      445      450      455
214  Val

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216 (2) INFORMATION FOR SEQ ID NO: 3:

217 (i) SEQUENCE CHARACTERISTICS:

218 (A) LENGTH: 591 base pairs

219 (B) TYPE: nucleic acid

220 (C) STRANDEDNESS: single

221 (D) TOPOLOGY: linear

W--> 222 (ii) MOLECULE TYPE: DNA

223 (ix) FEATURE:

224 (A) NAME/KEY: CDS

225 (B) LOCATION: 1..591

226 (ix) FEATURE:

227 (A) NAME/KEY: misc_feature

228 (D) OTHER INFORMATION: "rLBP25"

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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230  GCC AAC CCC GGC TTG GTC GCC AGG ATC ACC GAC AAG GGA CTG CAG TAT      48
231  Ala Asn Pro Gly Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr
232      1      5      10      15
233  GCG GCC CAG GAG GGG CTA TTG GCT CTG CAG AGT GAG CTG CTC AGG ATC      96
234  Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile
235      20      25      30
236  ACG CTG CCT GAC TTC ACC GGG GAC TTG AGG ATC CCC CAC GTC GGC CGT      144
237  Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg
238      35      40      45
239  GGG CGC TAT GAG TTC CAC AGC CTG AAC ATC CAC AGC TGT GAG CTG CTT      192
240  Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/994,185

DATE: 01/28/2002

TIME: 11:40:04

Input Set : N:\Crf3\RULE60\09994185.raw

Output Set: N:\CRF3\01282002\I994185.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:40 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1

L:222 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3